



1

SEQUENCE LISTING

<110> OSTERMEIER, MARC A.
GUNTAS, GURKAN

<120> METHODS FOR MAKING AND USING MOLECULAR SWITCHES
INVOLVING CIRCULAR PERMUTATION

<130> 71699/62568

<140> 10/588,114

<141> 2006-07-27

<150> PCT/US05/002633

<151> 2005-01-28

<150> 60/628,997

<151> 2004-11-18

<150> 60/607,684

<151> 2004-09-07

<150> 60/557,152

<151> 2004-03-26

<150> 60/539,774

<151> 2004-01-28

<160> 99

<170> PatentIn Ver. 3.3

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide linker

<400> 1

Gly Ser Gly Gly Gly
1 5

<210> 2

<211> 37

<212> PRT

<213> Homo sapiens

<400> 2

Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
1 5 10 15

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
20 25 30

Met Gly Leu Leu Thr
35

<210> 3
<211> 14
<212> PRT
<213> Rous sarcoma virus

<400> 3
Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg
1 5 10

<210> 4
<211> 25
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: GRK6 peptide
sequence

<400> 4
Leu Leu Gln Arg Leu Phe Ser Arg Gln Asp Cys Cys Gly Asn Cys Ser
1 5 10 15

Asp Ser Glu Glu Glu Leu Pro Thr Arg
20 25

<210> 5
<211> 7
<212> PRT
<213> Monkey virus SV40

<400> 5
Pro Lys Lys Lys Lys Lys Val
1 5

<210> 6
<211> 6
<212> PRT
<213> Homo sapiens

<400> 6
Ala Arg Arg Arg Arg Pro
1 5

<210> 7
<211> 10
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown: NF kappa-B p50
sequence

<400> 7

Glu Glu Val Gln Arg Lys Arg Gln Lys Leu
1 5 10

<210> 8

<211> 9

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown: NF kappa-B p65
sequence

<400> 8

Glu Glu Lys Arg Lys Arg Thr Tyr Glu
1 5

<210> 9

<211> 21

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown: Nucleoplasmin
sequence

<400> 9

Ala Val Lys Arg Pro Ala Ala Thr Leu Lys Lys Ala Gly Gln Ala Lys
1 5 10 15

Lys Lys Lys Leu Asp
20

<210> 10

<211> 5

<212> PRT

<213> Homo sapiens

<400> 10

Lys Phe Glu Arg Gln
1 5

<210> 11

<211> 36

<212> PRT

<213> Homo sapiens

<400> 11

Met Leu Ile Pro Ile Ala Gly Phe Phe Ala Leu Ala Gly Leu Val Leu
1 5 10 15

Ile Val Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly
 20 25 30

Tyr Gln Thr Ile
 35

<210> 12
 <211> 35
 <212> PRT
 <213> Homo sapiens

<400> 12
 Leu Val Pro Ile Ala Val Gly Ala Ala Leu Ala Gly Val Leu Ile Leu
 1 5 10 15

Val Leu Leu Ala Tyr Phe Ile Gly Leu Lys His His His Ala Gly Tyr
 20 25 30

Glu Gln Phe
 35

<210> 13
 <211> 27
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 13
 Met Leu Arg Thr Ser Ser Leu Phe Thr Arg Arg Val Gln Pro Ser Leu
 1 5 10 15

Phe Ser Arg Asn Ile Leu Arg Leu Gln Ser Thr
 20 25

<210> 14
 <211> 25
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 14
 Met Leu Ser Leu Arg Gln Ser Ile Arg Phe Phe Lys Pro Ala Thr Arg
 1 5 10 15

Thr Leu Cys Ser Ser Arg Tyr Leu Leu
 20 25

<210> 15
 <211> 64
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 15
 Met Phe Ser Met Leu Ser Lys Arg Trp Ala Gln Arg Thr Leu Ser Lys
 1 5 10 15

Ser Phe Tyr Ser Thr Ala Thr Gly Ala Ala Ser Lys Ser Gly Lys Leu
 20 25 30
 Thr Gln Lys Leu Val Thr Ala Gly Val Ala Ala Ala Gly Ile Thr Ala
 35 40 45
 Ser Thr Leu Leu Tyr Ala Asp Ser Leu Thr Ala Glu Ala Met Thr Ala
 50 55 60

<210> 16
 <211> 41
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 16
 Met Lys Ser Phe Ile Thr Arg Asn Lys Thr Ala Ile Leu Ala Thr Val
 1 5 10 15
 Ala Ala Thr Gly Thr Ala Ile Gly Ala Tyr Tyr Tyr Tyr Asn Gln Leu
 20 25 30
 Gln Gln Gln Gln Gln Arg Gly Lys Lys
 35 40

<210> 17
 <211> 4
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown: Endoplasmic
 reticulum localizing sequence

<400> 17
 Lys Asp Glu Leu
 1

<210> 18
 <211> 15
 <212> PRT
 <213> Human adenovirus type 19

<400> 18
 Leu Tyr Leu Ser Arg Arg Ser Phe Ile Asp Glu Lys Lys Met Pro
 1 5 10 15

<210> 19
 <211> 20
 <212> PRT
 <213> Unknown

<220>

<223> Description of Unknown: Interleukin-2
sequence

<400> 19

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser
20

<210> 20

<211> 29

<212> PRT

<213> Homo sapiens

<400> 20

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr
20 25

<210> 21

<211> 27

<212> PRT

<213> Homo sapiens

<400> 21

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1 5 10 15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn
20 25

<210> 22

<211> 18

<212> PRT

<213> Influenza A virus

<400> 22

Met Lys Ala Lys Leu Leu Val Leu Leu Tyr Ala Phe Val Ala Gly Asp
1 5 10 15

Gln Ile

<210> 23

<211> 24

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown: Interleukin-4
sequence

<400> 23

Met Gly Leu Thr Ser Gln Leu Leu Pro Pro Leu Phe Phe Leu Leu Ala
1 5 10 15

Cys Ala Gly Asn Phe Val His Gly
20

<210> 24

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 24

tgccgatcc ggcggtggcc acccagaaac gctggtg

37

<210> 25

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 25

gtctgaggat cccaatgct taatcagtga

30

<210> 26

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 26

gccgttaatc cagattac

18

<210> 27

<211> 41

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

 <220>
 <221> modified_base
 <222> (18)..(19)
 <223> a, c, g, t, unknown, or other

 <220>
 <221> modified_base
 <222> (21)..(22)
 <223> a, c, g, t, unknown, or other

 <400> 27
 gtaatctgga ttaaggcnnk nnkggtata acggtctgc t 41

 <210> 28
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <400> 28
 gaagataatg tcagggcc 18

 <210> 29
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

 <220>
 <221> modified_base
 <222> (19)..(20)
 <223> a, c, g, t, unknown, or other

 <400> 29
 ggccctgaca ttatcttcnn kgcacacgac cgctttggt 39

 <210> 30
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 30
aacagcgatc gggtaagc

18

<210> 31
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<220>
<221> modified_base
<222> (19)..(20)
<223> a, c, g, t, unknown, or other

<400> 31
gcttaccoga tcgctgttnn kgcgttatcg ctgatttat

39

<210> 32
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 32
cgggccggtg atgggtcat

18

<210> 33
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<220>
<221> modified_base
<222> (19)..(20)
<223> a, c, g, t, unknown, or other

<400> 33
atgaccatca acggcccgnn kgcgtgtcc aacatcgac

39

<210> 34
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 34

atccggacta gtaggccttt acttggtgat acgagt

36

<210> 35

<211> 1995

<212> DNA

<213> Escherichia coli

<400> 35

```

atgaaaataa aaacaggtgc acgcacccct gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatcct ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggttg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccoga tcgctgttga agcgttatcg 420
ctgattttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggttaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggg atggtccaac 780
atcgacacca gcaaagtga tttatgggtga acggtactgc cgaccttcaa ggttcaacca 840
tccaaaccgt tcgttggtgc gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaa cgtcggtgac cgtagcgtg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtaatg aagccatacc aaacgacgag cgtgacacca cgatgcctgc agcaatggca 1080
acaacgttgc gcaaactatt aactggcgaa ctacttactc tagcttcccg gcaacaatta 1140
atagactgga tggaggcgga taaagttgca ggaccacttc tgcgctcggc ccttcgggt 1200
ggctggttta ttgctgataa atctggagcc ggtgagcgtg ggtctcgcgg tatcattgca 1260
gcaactggggc cagatggtaa gccctcccgt atcgtagtta tctacacgac ggggagtcag 1320
tgaactatgg atgaacgaaa tagacagatc gctgagatag gtgcctcact gattaagcat 1380
tgggacaaga gccacccaga aacgctggtg aaagtaaaag atgctgaaga tcagttgggt 1440
gcacgagtgg gttacatcga actggatctc aacagcggtg agatccttga gagttttcgc 1500
cccgaagaac gttttccaat gatgagcact tttaaagttc tgctatgttg cgcggtatta 1560
tcccgtgttg acgcggggca agagcaactc ggtcgccgca tacactattc tcagaatgac 1620
ttggttgagt actcaccagt cacagaaaag catcttacgg atggcatgac agtaagagaa 1680
ttatgcagtg ctgccataac catgagtgat aacactgcgg ccaacttact tctgacaacg 1740
atcgaggagc cgaaggagct aaccgctttt ttgcacaaca tgggggatca tgtaactcgc 1800
cttgatcggt gggaaccgga actgaatgaa gccgcgcca ccatggaaaa cgcccagaaa 1860
ggtgaaatca tgccgaacat cccgcagatg tccgctttct ggtatgccgt gcgtactgcg 1920
gtgatcaacg ccgccagcgg tcgtcagact gtcgatgaag ccctgaaaga cgcgcagact 1980
cgtatcacca agtaa

```

<210> 36

<211> 664

<212> PRT

<213> Escherichia coli

<400> 36

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1                      5                      10                      15

```

Thr	Met	Met	Phe	Ser	Ala	Ser	Ala	Leu	Ala	Lys	Ile	Glu	Glu	Gly	Lys		
			20					25						30			
Leu	Val	Ile	Trp	Ile	Asn	Gly	Asp	Lys	Gly	Tyr	Asn	Gly	Leu	Ala	Glu		
		35					40					45					
Val	Gly	Lys	Lys	Phe	Glu	Lys	Asp	Thr	Gly	Ile	Lys	Val	Thr	Val	Glu		
	50					55					60						
His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	Pro	Gln	Val	Ala	Ala	Thr	Gly		
	65				70					75					80		
Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala	His	Asp	Arg	Phe	Gly	Gly	Tyr		
				85					90					95			
Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	Thr	Pro	Asp	Lys	Ala	Phe	Gln		
			100					105					110				
Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	Ala	Val	Arg	Tyr	Asn	Gly	Lys		
		115					120					125					
Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	Ala	Leu	Ser	Leu	Ile	Tyr	Asn		
	130					135					140						
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala		
	145				150					155					160		
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn		
				165				170						175			
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly		
			180					185					190				
Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly		
		195					200					205					
Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu		
	210					215					220						
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu		
	225				230					235					240		
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp		
				245					250					255			
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val		
			260					265					270				
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu		
		275					280						285				
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu		
	290					295					300						
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn		
	305				310					315					320		

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335
 Leu Ala Lys Asp Pro Arg Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp
 340 345 350
 Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr
 355 360 365
 Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met
 370 375 380
 Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala
 385 390 395 400
 Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg
 405 410 415
 Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val
 420 425 430
 Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg
 435 440 445
 Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser
 450 455 460
 His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
 465 470 475 480
 Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
 485 490 495
 Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
 500 505 510
 Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu
 515 520 525
 Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
 530 535 540
 Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
 545 550 555 560
 Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
 565 570 575
 Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
 580 585 590
 Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
 595 600 605
 Asn Glu Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met
 610 615 620

Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala
625 630 635 640

Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys
645 650 655

Asp Ala Gln Thr Arg Ile Thr Lys
660

<210> 37
<211> 1989
<212> DNA
<213> Escherichia coli

<400> 37
atgaaaataa aaacagggtgc acgcatcctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
aaaggctata acgggtctcg tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccgttg agcatccgga taaactggaa gagaaattcc cacagggttg ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgca tcgctgttga agcgttatcg 420
ctgattttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cggtcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctgggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa ggggtcaacca 840
tccaaaccgt tcgttggtg gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
ctggcgaaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtgcca taccaaacga cgagcgtgac accacgatgc ctgcagcaat ggcaacaacg 1080
ttgcgcaaac tattaactgg cgaactactt actctagctt cccggcaaca attaatagac 1140
tggatggagg cgataaaagt tgcaggacca cttctgcgct cggcccttcc ggctggctgg 1200
tttattgctg ataaatctgg agccggtgag cgtgggtctc gcggtatcat tgcagcactg 1260
gggccaatg gtaagccctc ccgtatcgta gttatctaca cgacggggag tcaggcaact 1320
atggatgaac gaaatagaca gatcgctgag ataggtgcct cactgattaa gcattgggac 1380
aagagccacc cagaaacgct ggtgaaagta aaagatgctg aagatcagtt ggggtgcacg 1440
gtgggttaca tcgaactgga tctcaacagc ggtaagatcc ttgagagttt tcgccccgaa 1500
gaacgttttc caatgatgag cactttttaa gttctgctat gtggcgcggt attatcccgt 1560
gttgacgccc ggcaagagca actcggctcg cgcatacact attctcagaa tgacttgggt 1620
gagtactcac cagtcacaga aaagcatctt acggatggca tgacagtaag agaattatgc 1680
agtgtgcca taaccatgag tgataacact gcggccaact tacttctgac aacgatcgg 1740
ggaccgaagg agctaaccgc ttttttgcac aacatggggg atcatgtaac tcgccttgat 1800
cggttgggaac cggaactgaa tgaagccgcc gccaccatgg aaaacgcca gaaagggtgaa 1860
atcatgccga acatcccga gatgtccgct ttctggtatg ccgtgcgtac tgcggtgatc 1920
aacgccgcca gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980
accaagtaa 1989

<210> 38
<211> 662
<212> PRT
<213> Escherichia coli

<400> 38

Met	Lys	Ile	Lys	Thr	Gly	Ala	Arg	Ile	Leu	Ala	Leu	Ser	Ala	Leu	Thr
1				5					10					15	
Thr	Met	Met	Phe	Ser	Ala	Ser	Ala	Leu	Ala	Lys	Ile	Glu	Glu	Gly	Lys
			20					25					30		
Leu	Val	Ile	Trp	Ile	Asn	Gly	Asp	Lys	Gly	Tyr	Asn	Gly	Leu	Ala	Glu
		35					40					45			
Val	Gly	Lys	Lys	Phe	Glu	Lys	Asp	Thr	Gly	Ile	Lys	Val	Thr	Val	Glu
	50					55					60				
His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	Pro	Gln	Val	Ala	Ala	Thr	Gly
65					70					75					80
Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala	His	Asp	Arg	Phe	Gly	Gly	Tyr
				85					90					95	
Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	Thr	Pro	Asp	Lys	Ala	Phe	Gln
			100					105					110		
Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	Ala	Val	Arg	Tyr	Asn	Gly	Lys
	115						120					125			
Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	Ala	Leu	Ser	Leu	Ile	Tyr	Asn
	130					135					140				
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala
145					150					155					160
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn
				165					170					175	
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly
			180					185					190		
Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly
	195						200					205			
Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu
	210					215					220				
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu
225					230					235					240
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp
				245					250					255	
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val
			260					265					270		
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu
		275					280					285			
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu
	290					295					300				

Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	
305					310					315					320	
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	
				325					330					335		
Leu	Ala	Lys	Asp	Pro	Arg	Ala	Ile	Pro	Asn	Asp	Glu	Arg	Asp	Thr	Thr	
			340					345					350			
Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu	
		355					360						365			
Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala	
		370				375					380					
Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	
385					390					395					400	
Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	
				405					410					415		
Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	
			420					425					430			
Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile	
		435					440					445				
Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro	
	450					455					460					
Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	
465					470					475					480	
Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	
				485				490						495		
Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	
			500					505					510			
Leu	Cys	Gly	Ala	Val	Leu	Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	
		515					520					525				
Gly	Arg	Arg	Ile	His	Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	
	530					535					540					
Val	Thr	Glu	Lys	His	Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	
545					550					555					560	
Ser	Ala	Ala	Ile	Thr	Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	
				565				570						575		
Thr	Thr	Ile	Gly	Gly	Pro	Lys	Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	
			580					585					590			
Gly	Asp	His	Val	Thr	Arg	Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	
		595					600					605				

Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
 610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
 625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
 645 650 655

Gln Thr Arg Ile Thr Lys
 660

<210> 39

<211> 1983

<212> DNA

<213> Escherichia coli

<400> 39

```

atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccoga tcgctgttga agcggtatcg 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtaa agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgctggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgacctcaa ggttcaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgtg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtccaa acgacgagcg tgacaccacg atgcctgcag caatggcaac aacgttgcgc 1080
aaactattaa ctggcgaaact acttactcta gcttcccggc aacaattaat agactggatg 1140
gaggcgata aagttgcagg accacttctg cgctcgccc ttccggctgg ctggtttatt 1200
gctgataaat ctggagccgg tgagcgtggg tctcgcggt tcatgcagc actggggcca 1260
gatggtaaag cctcccgtat cgtagttatc tacacgacgg ggagtcaggc aactatggat 1320
gaacgaaata gacagatcgc tgagataggt gcctcactga ttaagcattg ggacaagagc 1380
caccagaaa cgctggtgaa agtaaaagat gctgaagatc agttgggtgc acgagtgggt 1440
tacatcgaac tggatctcaa cagcggtaa atccttgaga gttttcgccc cgaagaacgt 1500
tttccaatga tgagcacttt taaagttctg ctatgtggcg cggtattatc ccgtgttgac 1560
gccgggcaag agcaactcgg tcgccgcata cactattctc agaatgactt ggttgagtac 1620
tcaccagtca cagaaaagca tcttacggat ggcatgacag taagagaatt atgcagtgt 1680
gccataacca tgagtataa cactgcggcc aacttacttc tgacaacgat cggaggaccg 1740
aaggagctaa ccgctttttt gcacaacatg ggggatcatg taactcgctc tgatcggttg 1800
gaaccggaac tgaatgaagc cgccgccacc atggaaaacg ccagaaagg tgaaatcatg 1860
ccgaacatcc cgcagatgtc cgctttctgg tatgccgtgc gtactgcggt gatcaacgcc 1920
gccagcggtc gtcagactgt cgatgaagcc ctgaaagacg cgcagactcg tatcaccaag 1980
taa
1983

```


<210> 40
 <211> 660
 <212> PRT
 <213> Escherichia coli

<400> 40
 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1 5 10 15
 Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 20 25 30
 Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
 35 40 45
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270

Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	275	280	285
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	290	295	300
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	305	310	315
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	325	330	335
Leu	Ala	Lys	Asp	Pro	Arg	Pro	Asn	Asp	Glu	Arg	Asp	Thr	Thr	Met	Pro	340	345	350
Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu	Leu	Leu	355	360	365
Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala	Asp	Lys	370	375	380
Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	Phe	Ile	385	390	395
Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	405	410	415
Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	420	425	430
Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	435	440	445
Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro	Glu	Thr	450	455	460
Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	465	470	475
Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	485	490	495
Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	500	505	510
Gly	Ala	Val	Leu	Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	515	520	525
Arg	Ile	His	Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	530	535	540
Glu	Lys	His	Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	545	550	555
Ala	Ile	Thr	Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	565	570	575

Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp
580 585 590

His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ala
595 600 605

Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro
610 615 620

Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala
625 630 635 640

Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr
645 650 655

Arg Ile Thr Lys
660

<210> 41
<211> 1986
<212> DNA
<213> Escherichia coli

<400> 41
atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggg aagaaattcg agaaagatac cggaattaaa 180
gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgga tcgctgttga agcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtaa agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcggtggg aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggg atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa ggggtcaacca 840
tccaaaccgt tcgttggtg gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtatac caaacgacga gcgtgacacc acgatgcctg cagcaatggc aacaacgctg 1080
cgaaactat taactggcga actacttact ctacttccc ggcaacaatt aatagactgg 1140
atggaggcgg ataaagtgc aggaccactt ctgcgctcgg ccttccggc tggctggttt 1200
attgctgata aatctggagc cggtagcggt gggctcgcg gtatcattgc agcaactggg 1260
ccagatggta agcctcccg tatcgtagtt atctacacga cggggagtca ggcaactatg 1320
gatgaacgaa atagacagat cgctgagata ggtgcctcac tgattaagca ttgggacaag 1380
agccacccag aaacgctggg gaaagtaaaa gatgctgaag atcagttggg tgcacgagt 1440
ggttacatcg aactggatct caacagcggg aagatccttg agagttttcg ccccgaaaga 1500
cgtttttcaa tgatgagcac ttttaaagtt ctgctatgtg gcgcggtatt atcccgtgtt 1560
gacgccgggc aagagcaact cggtcgcgcg atacactatt ctgagaatga cttgggttgag 1620
tactcaccag tcacagaaaa gcatcttacg gatggcatga cagtaagaga attatgcagt 1680
gctgccataa ccatgagtga taacactgcg gccaaacttac ttctgacaac gatcgaggga 1740
ccgaaggagc taaccgcttt tttgcacaac atgggggatc atgtaactcg ccttgatcgt 1800
tggaaccgg aactgaatga agccgcgcgc accatggaaa acgcccagaa aggtgaaatc 1860
atgccgaaca tccgcagat gccgcctttc tggtatgccc tgcgtactgc ggtgatcaac 1920
gccgccagcg gtcgtcagac tgctgatgaa gccctgaaag acgcgcagac tcgtatcacc 1980

aagtaa

1986

<210> 42
 <211> 661
 <212> PRT
 <213> Escherichia coli

<400> 42
 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1 5 10 15
 Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 20 25 30
 Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
 35 40 45
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255

Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val
			260					265					270		
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu
		275					280					285			
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu
	290					295					300				
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn
305					310					315					320
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu
				325					330					335	
Leu	Ala	Lys	Asp	Pro	Arg	Ile	Pro	Asn	Asp	Glu	Arg	Asp	Thr	Thr	Met
			340					345					350		
Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu	Leu
		355					360					365			
Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala	Asp
	370					375					380				
Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	Phe
385					390					395					400
Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile
				405					410					415	
Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr
			420					425					430		
Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala
		435					440					445			
Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro	Glu
	450					455					460				
Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val
465					470					475					480
Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe
				485					490					495	
Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu
			500					505					510		
Cys	Gly	Ala	Val	Leu	Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly
		515					520					525			
Arg	Arg	Ile	His	Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val
	530					535					540				
Thr	Glu	Lys	His	Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser
545					550					555					560

[illegible]

```
<210> 43
<211> 2001
<212> DNA
<213> Escherichia coli
```

<400>	43						
atgaaaataa	aaacaggtgc	acgcatacctc	gcattatccg	cattaacgac	gatgatgttt	60	
tccgcctcgg	ctctcgccaa	aatcgaagaa	ggtaaactgg	taatctggat	taacggcgat	120	
aaaggctata	acggtctcgc	tgaagtcggt	aagaaattcg	agaaagatac	cggaattaaa	180	
gtcaccgttg	agcatccgga	taaactggaa	gagaaattcc	cacaggttgc	ggcaactggc	240	
gatggccctg	acattatctt	ctgggcacac	gaccgcttgg	gtggctacgc	tcaatctcgg	300	
ctggttgctg	aaatcacccc	ggacaaagcg	ttccaggaca	agctgtatcc	gtttacctgg	360	
gatgccgtac	gttacaaacg	caagctgatt	gcttaccgca	tcgctgttga	agcgttatcg	420	
ctgatttata	acaaagatct	gctgccgaac	ccgccaaaaa	cctgggaaga	gatcccggcg	480	
ctggataaag	aactgaaagc	gaaaggtaag	agcgcgctga	tgttcaacct	gcaagaaccg	540	
tacttcacct	ggcgcgtgat	tgctgctgac	gggggttatg	cgttcaagta	tgaaaacggc	600	
aagtacgaca	ttaaagacgt	gggcgtggat	aacgctggcg	cgaagcggg	tctgaccttc	660	
ctggttaatg	aagccatacc	aaacgacgag	cgtgacacca	cgatgcctgc	agcaatggca	720	
acaacgttgc	gcaaactatt	aactggcgaa	ctacttactc	tagcttcccg	gcaacaatta	780	
atagactgga	tggaggcgga	taaagttgca	ggaccacttc	tgcgctcggc	ccttcgggct	840	
ggctggttta	ttgctgataa	atctggagcc	ggtgagcgtg	ggtctcgcgg	tatcattgca	900	
gcactggggc	cagatggtaa	gccctcccgt	atcgtagtta	tctacacgac	ggggagtcag	960	
gcaactatgg	atgaacgaaa	tagacagatc	gctgagatag	gtgcctcact	gattaagcat	1020	
tgggacaaga	gccaccgaga	aacgtggtg	aaagtaaaag	atgctgaaga	tcagttgggt	1080	
gcacgagtgg	gttacatcga	actggatctc	aacagcggta	agatccttga	gagttttcgc	1140	
cccgaagaac	gtttttccaat	gatgagcact	tttaaagttc	tgctatgtgg	cgcggtatta	1200	
tcccgtgttg	acgcgcggca	agagcaactc	ggtcgccgca	tacactattc	tcagaatgac	1260	
ttggttgagt	actcaccagt	cacagaaaag	catcttacgg	atggcatgac	agtaagagaa	1320	
ttatgcagtg	ctgccataac	catgagtgat	aacactgcgg	ccaacttact	tctgacaacg	1380	
atcggaggac	cgaaggagct	aaccgctttt	ttgcacaaca	tgggggatca	tgtaactcgc	1440	
cttgatcggt	gggaaccgga	actgaatgaa	gccgttgacc	tgattaaaaa	caaacacatg	1500	
aatgcagaca	ccgattactc	catcgcaaga	gctgccttta	ataaaggcga	aacagcgatg	1560	
accatcaacg	gcccgtgggc	atggtccaac	atcgacacca	gcaaagtgaa	ttatgggtga	1620	
acggtactcg	cgaccttcaa	gggtcaacca	tccaaaccgt	tcgttggcgt	gctgagcgca	1680	
ggtattaacg	ccgcagctcc	gaacaaagag	ctggcgaaaag	agttctctcg	aaactatctg	1740	
ctgactgatg	aaggtctgga	agcggttaat	aaagacaaac	cgctgggtgc	cgtagcgctg	1800	

```

aagtcttacg aggaagagtt ggcgaaagat ccacgtattg ccgccaccat ggaaaacgcc 1860
cagaaagggtg aaatcatgcc gaacatccccg cagatgtccg ctttctggta tgccgtgcgt 1920
actgcggtga tcaacgccgc cagcgtcgt cagactgtcg atgaagccct gaaagacgcg 1980
cagactcgta tcaccaagta a 2001

```

<210> 44

<211> 666

<212> PRT

<213> Escherichia coli

<400> 44

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1                      5                      10                      15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
          20                      25                      30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
          35                      40                      45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
          50                      55                      60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
          65                      70                      75                      80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
          85                      90                      95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
          100                      105                      110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
          115                      120                      125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
          130                      135                      140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
          145                      150                      155                      160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
          165                      170                      175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
          180                      185                      190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
          195                      200                      205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asn Glu
          210                      215                      220

Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Ala Ala Met Ala
          225                      230                      235                      240

```

Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu	Leu	Leu	Thr	Leu	Ala	Ser	
				245					250					255		
Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala	Asp	Lys	Val	Ala	Gly	Pro	
			260					265					270			
Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	Phe	Ile	Ala	Asp	Lys	Ser	
		275					280					285				
Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	
	290					295					300					
Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	
305					310					315					320	
Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	
				325					330					335		
Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro	Glu	Thr	Leu	Val	Lys	Val	
			340					345					350			
Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	
		355					360					365				
Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	
	370					375					380					
Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly	Ala	Val	Leu	
385					390					395					400	
Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg	Ile	His	Tyr	
				405					410					415		
Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	Glu	Lys	His	Leu	
			420					425					430			
Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	Ala	Ile	Thr	Met	
		435					440					445				
Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	Ile	Gly	Gly	Pro	
	450					455					460					
Lys	Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	Gly	Asp	His	Val	Thr	Arg	
465					470					475					480	
Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	Ala	Val	Asp	Leu	Ile	Lys	
				485					490					495		
Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	
			500					505					510			
Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	
		515					520					525				
Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	
	530					535					540					

Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser Ala
545 550 555 560

Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu
565 570 575

Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys Asp
580 585 590

Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala
595 600 605

Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu
610 615 620

Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg
625 630 635 640

Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala
645 650 655

Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys
660 665

<210> 45

<211> 1989

<212> DNA

<213> Escherichia coli

<400> 45

```

atgaaaataa aaacagggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccggtt agcatccgga taaactggaa gagaaattcc cacagggtgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctggttggtg aaatcacccc ggacaaaagc ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccoga tgcgtgttga agcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctgggttgacc tgattaatga agccatacca aacgacgagc gtgacaccac gatgcctgca 720
gcaatggcaa caacgttgcg caaactatta actggcgaac tacttactct agcttcccgg 780
caacaattaa tagactggat ggaggcggat aaagttgcag gaccatttct gcgctcggcc 840
cttccggctg gctggtttat tgctgataaa tctggagccg gtgagcgtgg gtctcgcggg 900
atcattgcag cactggggcc agatggtaag cctcccgtta tcgtagttat ctacacgacg 960
gggagtcagg caactatgga tgaacgaaat agacagatcg ctgagatagg tgcctcactg 1020
attaagcatt gggacaagag ccaccagaa acgctgggtg aagtaaaaga tgctgaagat 1080
cagttgggtg cacgagtggg ttacatcgaa ctggatctca acagcggtaa gatccttgag 1140
agttttcgcc ccgaagaacg ttttccaatg atgagcactt ttaaagttct gctatgtggc 1200
gcggtattat cccgtgttga cgccgggcaa gagcaactcg gtcgccgcat acactattct 1260
cagaatgact tggttgagta ctcaccagtc acagaaaagc atcttacgga tggcatgaca 1320
gtaagagaat tatgcagtgc tgccataacc atgagtgata aactgcggc caacttactt 1380
ctgacaacga tcggaggacc gaaggagcta accgcttttt tgcacaacat gggggatcat 1440
gtaactcgcc ttgatcggtt ggaaccggaa ctgaatgaag cccacatgaa tgcagacacc 1500
gattactcca tcgcagaagc tgcctttaat aaaggcgaaa cagcgatgac catcaacggc 1560
ccgtgggcat ggtccaacat cgacaccagc aaagtgaatt atggtgtaac ggtactgccg 1620

```

```

accttcaagg gtcaaccatc caaaccggtc gttggcggtgc tgagcgcagg tattaacgcc 1680
gccagtccga acaaagagct ggcgaaagag ttcctcgaaa actatctgct gactgatgaa 1740
ggtctggaag cggttaataa agacaaaccg ctgggtgccg tagcgtgaa gtcttacgag 1800
gaagagttgg cgaaagatcc acgtattgcc gccaccatgg aaaacgcca gaaaggtgaa 1860
atcatgccga acatccccga gatgtccgct ttctggtatg ccgtgcgtac tgcggtgac 1920
aacgccgcca gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980
accaagtaa

```

```

<210> 46
<211> 662
<212> PRT
<213> Escherichia coli

```

```

<400> 46
Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1              5              10              15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20              25              30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35              40              45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50              55              60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65              70              75              80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85              90              95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100             105             110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
      115             120             125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
      130             135             140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
      145             150             155             160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
      165             170             175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
      180             185             190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
      195             200             205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
      210             215             220

```

Ile	Asn	Glu	Ala	Ile	Pro	Asn	Asp	Glu	Arg	Asp	Thr	Thr	Met	Pro	Ala
225					230					235					240
Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu	Leu	Leu	Thr
				245					250					255	
Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala	Asp	Lys	Val
			260					265					270		
Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	Phe	Ile	Ala
		275					280					285			
Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala
	290					295					300				
Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr
305					310					315					320
Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile
				325					330					335	
Gly	Ala	Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro	Glu	Thr	Leu
			340					345					350		
Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr
		355					360					365			
Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro
	370					375					380				
Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly
385					390					395					400
Ala	Val	Leu	Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg
				405				410						415	
Ile	His	Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	Glu
			420					425					430		
Lys	His	Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	Ala
		435					440					445			
Ile	Thr	Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	Ile
	450					455					460				
Gly	Gly	Pro	Lys	Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	Gly	Asp	His
465					470					475					480
Val	Thr	Arg	Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	Ala	His	Met
				485					490					495	
Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	Lys	Gly
			500					505					510		
Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	Ile	Asp
		515					520					525			

Thr Ser Lys Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly
 530 535 540
 Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala
 545 550 555 560
 Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu
 565 570 575
 Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly
 580 585 590
 Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg
 595 600 605
 Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
 610 615 620
 Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
 625 630 635 640
 Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
 645 650 655
 Gln Thr Arg Ile Thr Lys
 660

<210> 47
 <211> 1989
 <212> DNA
 <213> Escherichia coli

<400> 47
 atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
 tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
 aaaggctata acggtctcgc tgaagtcggg aagaaattcg agaaagatac cggaattaaa 180
 gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctggttgctg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttaccgca tgcgtgttga agcgttatcg 420
 ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
 ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
 tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
 aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
 ctgggtgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaa 720
 gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atggtccaac 780
 atcgacacca gcaaagtga tttatggtgta acggtactgc cgaccttcaa gggtaacca 840
 tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
 ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
 aaagacaaac cgctgggtgc cgtagcgtcg aagtcttacg aggaagagtt ggcgaaagat 1020
 ccacgtaatg aagccatacc aaacgacgag cgtgacacca cgatgcctgc agcaatggca 1080
 acaacgttgc gcaaactatt aactggcgaa ctacttactc tagcttcccg gcaacaatta 1140
 atagactgga tggaggcgga taaagttgca ggaccacttc tgcgctcggc ccttccggct 1200
 ggctggttta ttgctgataa atctggagcc ggtgagcgtg ggtctcgcgg tatcattgca 1260
 gcaactggggc cagatggtaa gccctcccgt atcgtagtta tctacacgac ggggagtcag 1320
 gcaactatgg atgaacgaaa tagacagatc gctgagatag gtgcctcact gattaagcat 1380
 tgggacaaga gccaccaga aacgctgggtg aaagtaaaag atgctgaaga tcagttgggt 1440

```

gcacgagtggt gttacatcga actggatctc aacagcggta agatccttga gagtttttcgc 1500
cccgaagaac gttttccaat gatgagcact tttaaagtgc tgctatgtgg cgcggtatta 1560
tcccgtgttg acgcccggca agagcaactc ggtcgccgca tacactattc tcagaatgac 1620
ttgggttgagt actcaccagt cacagaaaag catcttacgg atggcatgac agtaagagaa 1680
ttatgcagtg ctgccataac catgagtgat aacactgcgg ccaacttact tctgacaacg 1740
atcggaggac cgaaggagct aaccgctttt ttgcacaaca tgggggatca tgtaactcgc 1800
cttgatcggt gggaaccgga actgaatgaa gccaccatgg aaaacgcca gaaaggtgaa 1860
atcatgccga acatcccgca gatgtccgct ttctggtagt ccgtgcgtac tgcggtgatc 1920
aacgccgcca gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980
accaagtaa                                     1989

```

<210> 48

<211> 662

<212> PRT

<213> Escherichia coli

<400> 48

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1                      5                      10                      15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
          20                      25                      30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
          35                      40                      45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
          50                      55                      60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
          65                      70                      75                      80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
          85                      90                      95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
          100                     105                     110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
          115                     120                     125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
          130                     135                     140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
          145                     150                     155                     160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
          165                     170                     175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
          180                     185                     190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
          195                     200                     205

```

Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	210	215	220	
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	225	230	235	240
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	245	250	255	
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	260	265	270	
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	275	280	285	
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	290	295	300	
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	305	310	315	320
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	325	330	335	
Leu	Ala	Lys	Asp	Pro	Arg	Asn	Glu	Ala	Ile	Pro	Asn	Asp	Glu	Arg	Asp	340	345	350	
Thr	Thr	Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	355	360	365	
Gly	Glu	Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	370	375	380	
Glu	Ala	Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	385	390	395	400
Gly	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	405	410	415	
Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	420	425	430	
Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	435	440	445	
Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	450	455	460	
His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	465	470	475	480
Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	485	490	495	
Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	500	505	510	

Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu
515 520 525

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
530 535 540

Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
545 550 555 560

Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
565 570 575

Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
580 585 590

Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
595 600 605

Asn Glu Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
645 650 655

Gln Thr Arg Ile Thr Lys
660

<210> 49
<211> 2007
<212> DNA
<213> Escherichia coli

<400> 49
atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctggttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgga tcgctgttga agcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcggtgat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa gggtaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
ctggcgaaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgtg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtattg ccgccaccaa tgaagccata ccaaacgacg agcgtgacac cacgatgcct 1080
gcagcaatgg caacaacgtt gcgcaacta ttaactggcg aactacttac tctagcttcc 1140
cggcaacaat taatagactg gatggaggcg gataaagtg caggaccact tctgcgtcgc 1200
gcccttccgg ctggctggtt tattgctgat aaatctggag ccggtgagcg tgggtctcgc 1260

```

ggatcattg cagcactggg gccagatggt aagccctccc gtatcgtagt tatctacacg 1320
acgggggagtc aggcaactat ggatgaacga aatagacaga tcgctgagat aggtgcctca 1380
ctgattaagc attgggacaa gagccaccca gaaacgctgg tgaaagtaaa agatgctgaa 1440
gatcagttgg gtgcacgagt gggttacatc gaactggatc tcaacagcgg taagatcctt 1500
gagagttttc gccccgaaga acgttttcca atgatgagca cttttaaaagt tctgctatgt 1560
ggcgcggtat tatcccggtg tgacgccggg caagagcaac tcggtcgccg catacactat 1620
tctcagaatg acttggttga gtactcacca gtcacagaaa agcatccttac ggatggcatg 1680
acagtaagag aattatgcag tgctgccata accatgagtg ataacactgc ggccaactta 1740
cttctgacaa cgatcggagg accgaaggag ctaaccgctt ttttgacaaa catgggggat 1800
catgtaactc gccttgatcg ttgggaaccg gaactgaatg aagccgccgc caccatggaa 1860
aacgcccaga aaggtgaaat catgccgaac atccgcgaga tgtccgcttt ctggtatgcc 1920
gtgcgtactg cggatgatcaa cgccgccagc ggctcgcaga ctgtcgatga agccctgaaa 1980
gacgcgcaga ctcgatcac caagtaa 2007

```

<210> 50
 <211> 668
 <212> PRT
 <213> Escherichia coli

<400> 50
 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1 5 10 15
 Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 20 25 30
 Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
 35 40 45
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190

Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	195	200	205
Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	210	215	220
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	225	230	235
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	245	250	255
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	260	265	270
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	275	280	285
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	290	295	300
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	305	310	315
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	325	330	335
Leu	Ala	Lys	Asp	Pro	Arg	Ile	Ala	Ala	Thr	Asn	Glu	Ala	Ile	Pro	Asn	340	345	350
Asp	Glu	Arg	Asp	Thr	Thr	Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	355	360	365
Lys	Leu	Leu	Thr	Gly	Glu	Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	370	375	380
Ile	Asp	Trp	Met	Glu	Ala	Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	385	390	395
Ala	Leu	Pro	Ala	Gly	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	405	410	415
Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	420	425	430
Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	435	440	445
Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	450	455	460
Trp	Asp	Lys	Ser	His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	465	470	475
Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	485	490	495

Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met
 500 505 510
 Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp
 515 520 525
 Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp
 530 535 540
 Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met
 545 550 555 560
 Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr
 565 570 575
 Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr
 580 585 590
 Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp
 595 600 605
 Glu Pro Glu Leu Asn Glu Ala Ala Ala Thr Met Glu Asn Ala Gln Lys
 610 615 620
 Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala
 625 630 635 640
 Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp
 645 650 655
 Glu Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys
 660 665

<210> 51
 <211> 1989
 <212> DNA
 <213> Escherichia coli

<400> 51
 atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
 tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
 aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
 gtcaccggtg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctggttgctg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttaccgga tcgctgttga agcggtatcg 420
 ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
 ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
 tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
 aagtacgaca ttaaagacgt gggcgctggat aacgctggcg cgaaagcggg tctgaccttc 660
 ctgggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaaa 720
 gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atggtccaac 780
 atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa ggggtcaacca 840
 tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
 ctggcgaaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
 aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020
 ccacgtaatg aagccatacc aaacgacgag cgtgacacca cgatgcctgc agcaatggca 1080

```

acaacgttgc gcaaactatt aactggcgaa ctacttactc tagcttcccg gcaacaatta 1140
atagactgga tggaggcgga taaagttgca ggaccacttc tgcgctcggc cttccgggt 1200
ggctgggttta ttgctgataa atctggagcc ggtgagcgtg ggtctcgcgg tatcattgca 1260
gcactggggc cagatggtaa gccctcccgt atcgtagtta tctacacgac ggggagtcag 1320
gcaactatgg atgaacgaaa tagacagatc gctgagatag gtgcctcact gattaagcat 1380
tgggacaaga gccacccaga aacgctggtg aaagtaaaag atgctgaaga tcagttgggt 1440
gcacgagtgg gttacatcga actggatctc aacagcggta agatccttga gagttttcgc 1500
cccgaagaac gttttccaat gatgagcact tttaaagttc tgctatgtgg cgcggtatta 1560
tcccgtggtg acgccgggca agagcaactc ggtcgcgcga tacactattc tcagaatgac 1620
ttggttgagt actcaccagt cacagaaaag catcttacgg atggcatgac agtaagagaa 1680
ttatgcagtg ctgccataac catgagtgat aacactgcgg ccaacttact tctgacaacg 1740
atcgaggagc cgaaggagct aaccgctttt ttgcacaaca tgggggatca tgtaactcgc 1800
cttgatcggt gggaaccgga actgaatgaa gccaccatgg aaaacgcca gaaaggtgaa 1860
atcatgccga acatcccgcga gatgtccgct ttctggtatg ccgtgcgtac tgcggtgatc 1920
aacgccgcca gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980
accaagtaa 1989

```

<210> 52
 <211> 662
 <212> PRT
 <213> Escherichia coli

<400> 52
 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1 5 10 15
 Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 20 25 30
 Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
 35 40 45
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175

Leu	Gln	Glu	Pro 180	Tyr	Phe	Thr	Trp	Pro 185	Leu	Ile	Ala	Ala	Asp 190	Gly	Gly
Tyr	Ala	Phe 195	Lys	Tyr	Glu	Asn	Gly 200	Lys	Tyr	Asp	Ile	Lys 205	Asp	Val	Gly
Val	Asp 210	Asn	Ala	Gly	Ala	Lys 215	Ala	Gly	Leu	Thr	Phe 220	Leu	Val	Asp	Leu
Ile 225	Lys	Asn	Lys	His	Met 230	Asn	Ala	Asp	Thr	Asp 235	Tyr	Ser	Ile	Ala	Glu 240
Ala	Ala	Phe	Asn	Lys 245	Gly	Glu	Thr	Ala	Met 250	Thr	Ile	Asn	Gly	Pro 255	Trp
Ala	Trp	Ser	Asn 260	Ile	Asp	Thr	Ser	Lys 265	Val	Asn	Tyr	Gly	Val 270	Thr	Val
Leu	Pro	Thr 275	Phe	Lys	Gly	Gln	Pro 280	Ser	Lys	Pro	Phe	Val 285	Gly	Val	Leu
Ser	Ala 290	Gly	Ile	Asn	Ala	Ala 295	Ser	Pro	Asn	Lys	Glu 300	Leu	Ala	Lys	Glu
Phe 305	Leu	Glu	Asn	Tyr	Leu 310	Leu	Thr	Asp	Glu	Gly 315	Leu	Glu	Ala	Val	Asn 320
Lys	Asp	Lys	Pro	Leu 325	Gly	Ala	Val	Ala	Leu 330	Lys	Ser	Tyr	Glu	Glu 335	Glu
Leu	Ala	Lys	Asp 340	Pro	Arg	Asn	Glu	Ala 345	Ile	Pro	Asn	Asp	Glu 350	Arg	Asp
Thr	Thr	Met 355	Pro	Ala	Ala	Met	Ala 360	Thr	Thr	Leu	Arg	Lys 365	Leu	Leu	Thr
Gly	Glu 370	Leu	Leu	Thr	Leu	Ala 375	Ser	Arg	Gln	Gln	Leu 380	Ile	Asp	Trp	Met
Glu 385	Ala	Asp	Lys	Val	Ala 390	Gly	Pro	Leu	Leu	Arg 395	Ser	Ala	Leu	Pro	Ala 400
Gly	Trp	Phe	Ile	Ala 405	Asp	Lys	Ser	Gly	Ala 410	Gly	Glu	Arg	Gly	Ser 415	Arg
Gly	Ile	Ile	Ala 420	Ala	Leu	Gly	Pro	Asp 425	Gly	Lys	Pro	Ser	Arg 430	Ile	Val
Val	Ile	Tyr 435	Thr	Thr	Gly	Ser	Gln 440	Ala	Thr	Met	Asp	Glu 445	Arg	Asn	Arg
Gln	Ile	Ala	Glu	Ile	Gly	Ala 455	Ser	Leu	Ile	Lys	His 460	Trp	Asp	Lys	Ser
His 465	Pro	Glu	Thr	Leu	Val 470	Lys	Val	Lys	Asp	Ala 475	Glu	Asp	Gln	Leu	Gly 480

Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
485 490 495

Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
500 505 510

Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu
515 520 525

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
530 535 540

Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
545 550 555 560

Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
565 570 575

Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
580 585 590

Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
595 600 605

Asn Glu Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
645 ; 650 655

Gln Thr Arg Ile Thr Lys
660

<210> 53

<211> 1989

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 53

```

atgaaaataa aaacaggtgc acgcatactc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcttg 120
tttggtata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctatgcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggtcg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgga tcgctgttta tgcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgcaaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtgaa agcgcgctga tggtcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660

```

```

ctgggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atgggtccaac 780
atcgacacca gcaaagtga ttatgggtgta acggtactgc cgaccttcaa gggtaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
ctggcgaaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtgcca taccaaacga cgagcgtgac accacgatgc ctgcagcaat ggcaacaacg 1080
ttgcgcaaac tattaactgg cgaactactt actctagctt cccggcaaca attaatagac 1140
tggatggagg cggataaagt tgcaggacca cttctgcgt cggcccttcc ggctggctgg 1200
tttattgctg ataaatctgg agccggtgag cgtgggtctc gcggtatcat tgcagcactg 1260
gggccagatg gtaagccctc ccgtatcgta gttatctaca cgacggggag tcaggcaact 1320
atggatgaac gaaatagaca gatcgctgag ataggtgcct cactgattaa gcattgggac 1380
aagagccacc cagaaacgct ggtgaaagta aaagatgctg aagatcagtt gggatgcacga 1440
gtgggttaca tcgaactgga tctcaacagc ggtaagatcc ttgagagttt tcgccccgaa 1500
gaacgttttc caatgatgag cacttttaaa gttctgctat gtggcgcggt attatcccgt 1560
gttgacgccg ggcaagagca actcgggtcg cgcatacact attctcagaa tgacttggtt 1620
gagtactcac cagtcacaga aaagcatctt acggatggca tgacagtaag agaattatgc 1680
agtgtcgcca taaccatgag tgataacact gcggccaact tacttctgac aacgatcgga 1740
ggaccgaagg agctaaccgc ttttttgac aacatggggg atcatgtaac tcgccttgat 1800
cgttgggaac cggaactgaa tgaagccgcc gccaccatgg aaaacgcccga gaaaggtgaa 1860
atcatgccga acatcccgcga gatgtccgct ttctggtatg ccgtgcgtac tgcggtgatc 1920
aacgccgcca gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980
accaagtaa 1989

```

<210> 54

<211> 662

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic protein construct

<400> 54

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1                      5                      10          15

```

```

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20                      25          30

```

```

Leu Val Ile Trp Ile Asn Gly Leu Phe Gly Tyr Asn Gly Leu Ala Glu
    35                      40          45

```

```

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
    50                      55          60

```

```

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
    65                      70          75          80

```

```

Asp Gly Pro Asp Ile Ile Phe Tyr Ala His Asp Arg Phe Gly Gly Tyr
      85                      90          95

```

```

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
    100                      105          110

```

```

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
    115                      120          125

```

Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Tyr	Ala	Leu	Ser	Leu	Ile	Tyr	Asn	130	135	140		
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala	145	150	155	160	
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn	165	170		175	
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly	180	185		190	
Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	195	200		205	
Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	210	215		220	
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	225	230		235	240
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	245	250		255	
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	260	265		270	
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	275	280		285	
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	290	295		300	
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	305	310	315	320	
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	325	330		335	
Leu	Ala	Lys	Asp	Pro	Arg	Ala	Ile	Pro	Asn	Asp	Glu	Arg	Asp	Thr	Thr	340	345		350	
Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu	355	360		365	
Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala	370	375		380	
Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	385	390	395	400	
Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	405	410		415	
Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	420	425		430	

[illegible]

```
<210> 55
<211> 662
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic protein construct

<400> 55
Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
1 5 10 15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 20 25 30

Leu Val Ile Trp Ile Asn Gly Leu Gln Gly Tyr Asn Gly Leu Ala Glu
 35 40 45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80

Asp Gly Pro Asp Ile Ile Phe Tyr Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125

Leu Ile Ala Tyr Pro Ile Ala Val Gln Ala Leu Ser Leu Ile Tyr Asn
 130 135 140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205

Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220

Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240

Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255

Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270

Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285

Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300

Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320

Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335
 Leu Ala Lys Asp Pro Arg Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr
 340 345 350
 Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu
 355 360 365
 Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala
 370 375 380
 Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp
 385 390 395 400
 Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile
 405 410 415
 Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile
 420 425 430
 Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile
 435 440 445
 Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Asp Lys Ser His Pro
 450 455 460
 Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg
 465 470 475 480
 Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser
 485 490 495
 Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu
 500 505 510
 Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu
 515 520 525
 Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro
 530 535 540
 Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys
 545 550 555 560
 Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu
 565 570 575
 Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met
 580 585 590
 Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu
 595 600 605
 Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
 610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
645 650 655

Gln Thr Arg Ile Thr Lys
660

<210> 56
<211> 1989
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 56
atgaaaataa aaacagggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcaag 120
gagggctata acgggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcacccgttg agcatccgga taaactggaa gagaaattcc cacagggtgc ggcaactggc 240
gatggccctg acattatctt ctatgcacac gaccgctttg gtggctacgc tcaatctggc 300
ctggttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgca tcgctgttcg ggcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcggtgat aacgctggcg cgaaagcggg tctgaccttc 660
ctgggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcgaaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa gggtaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtc gaacaaagag 900
ctggcgaaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtgccca taccaaacga cgagcgtgac accacgatgc ctgcagcaat ggcaacaacg 1080
ttgcgcaaac tattaactgg cgaactactt actctagctt cccggcaaca attaatagac 1140
tggatggagg cggataaagt tgcaggacca ctctcgcgt cgcccttcc ggctggctgg 1200
tttattgctg ataaatctgg agccggtgag cgtgggtctc gcggtatcat tgcagcactg 1260
gggccagatg gtaagccctc ccgtatcgta gttatctaca cgacggggag tcaggcaact 1320
atggatgaac gaaatagaca gatcgctgag ataggtgcct cactgattaa gcattgggac 1380
aagagccacc cagaaacgct ggtgaaagta aaagatgctg aagatcagtt ggggtgcacga 1440
gtgggttaca tcgaactgga tctcaacagc ggtaagatcc ttgagagttt tcgccccgaa 1500
gaacgttttc caatgatgag cactttttaa gttctgctat gtggcgcggt attatcccg 1560
gttgacgcgg ggcaagagca actcggtcgc cgcatacact attctcagaa tgacttggtt 1620
gagtactcac cagtcacaga aaagcatctt acggatggca tgacagtaag agaattatgc 1680
agtgtgcca taaccatgag tgataacact gcggccaact tacttctgac aacgatcgga 1740
ggaccgaagg agctaaccgc ttttttgac aacatggggg atcatgtaac tcgccttgat 1800
cgttgggaac cggaactgaa tgaagccgcc gccaccatgg aaaacgcca gaaagggtgaa 1860
atcatgccga acatcccgcga gatgtccgct ttctggtatg ccgtgcgtac tgcggtgatc 1920
aacgccgcca gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980
accaagtaa 1989

<210> 57
 <211> 662
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 protein construct

<400> 57

Met	Lys	Ile	Lys	Thr	Gly	Ala	Arg	Ile	Leu	Ala	Leu	Ser	Ala	Leu	Thr	1	5	10	15
Thr	Met	Met	Phe	Ser	Ala	Ser	Ala	Leu	Ala	Lys	Ile	Glu	Glu	Gly	Lys	20	25	30	
Leu	Val	Ile	Trp	Ile	Asn	Gly	Lys	Glu	Gly	Tyr	Asn	Gly	Leu	Ala	Glu	35	40	45	
Val	Gly	Lys	Lys	Phe	Glu	Lys	Asp	Thr	Gly	Ile	Lys	Val	Thr	Val	Glu	50	55	60	
His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	Pro	Gln	Val	Ala	Ala	Thr	Gly	65	70	75	80
Asp	Gly	Pro	Asp	Ile	Ile	Phe	Tyr	Ala	His	Asp	Arg	Phe	Gly	Gly	Tyr	85	90	95	
Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	Thr	Pro	Asp	Lys	Ala	Phe	Gln	100	105	110	
Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	Ala	Val	Arg	Tyr	Asn	Gly	Lys	115	120	125	
Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Arg	Ala	Leu	Ser	Leu	Ile	Tyr	Asn	130	135	140	
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala	145	150	155	160
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn	165	170	175	
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly	180	185	190	
Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	195	200	205	
Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	210	215	220	
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	225	230	235	240
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	245	250	255	

Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	260	265	270
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	275	280	285
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	290	295	300
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	305	310	315
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	325	330	335
Leu	Ala	Lys	Asp	Pro	Arg	Ala	Ile	Pro	Asn	Asp	Glu	Arg	Asp	Thr	Thr	340	345	350
Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu	355	360	365
Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala	370	375	380
Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	385	390	395
Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	405	410	415
Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	420	425	430
Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile	435	440	445
Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro	450	455	460
Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	465	470	475
Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	485	490	495
Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	500	505	510
Leu	Cys	Gly	Ala	Val	Leu	Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	515	520	525
Gly	Arg	Arg	Ile	His	Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	530	535	540
Val	Thr	Glu	Lys	His	Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	545	550	555

Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu
565 570 575

Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met
580 585 590

Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu
595 600 605

Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
610 615 620

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
645 650 655

Gln Thr Arg Ile Thr Lys
660

<210> 58

<211> 1989

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 58

```

atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaacttg taatctggat taacggcttg 120
gagggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcacccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctatgcacac gaccgctttg gtggctacgc tcaatctggc 300
ctggttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgca tcgctgttcg tgcgttatcg 420
ctgatttata acaagatctt gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tggtcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggg atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa gggtaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgtcg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtgcc aaccaaacga cgagcgtgac accacgatgc ctgcagcaat ggcaacaacg 1080
ttgcgcaaac tattaactgg cgaactactt actctagctt cccggcaaca attaatagac 1140
tggatggagg cgataaaagt tgcaggacca cttctgcgct cggcccttcc ggctggctgg 1200
tttattgctg ataaatctgg agccggtgag cgtgggtctc gcggtatcat tgcagcactg 1260
gggccagatg gtaagccctc ccgtatcgta gttatctaca cgacggggag tcaggcaact 1320
atggatgaac gaaatagaca gatcgctgag ataggtgcct cactgattaa gcattgggac 1380
aagagccacc cagaaacgct ggtgaaagta aaagatgctg aagatcagtt gggcgacga 1440
gtgggttaca tcgaactgga tctcaacagc ggtaagatcc ttgagagttt tcgccccgaa 1500
gaacggtttc caatgatgag cactttttaa gttctgctat gtggcgcggt attatcccgt 1560

```

```

gttgacgccg ggcaagagca actcgggtcgc cgcatacaact attctcagaa tgacttgggtt 1620
gagtactcac cagtcacaga aaagcatctt acggatggca tgacagtaag agaattatgc 1680
agtgtctgcca taaccatgag tgataaact gcggccaact tacttctgac aacgatcgga 1740
ggaccgaagg agctaaccgc ttttttgac aacatggggg atcatgtaac tcgccttgat 1800
cgttgggaac cggaactgaa tgaagccgcc gccaccatgg aaaacgcca gaaaggtgaa 1860
atcatgccga acatcccgc gatgtccgct ttctggtatg ccgtgcgtac tgcggtgatc 1920
aacgccgcca gcggtcgtca gactgtcgat gaagccctga aagacgcgca gactcgtatc 1980
accaagtaa                                     1989

```

<210> 59

<211> 662

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 59

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1             5             10             15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
          20             25             30

Leu Val Ile Trp Ile Asn Gly Leu Glu Gly Tyr Asn Gly Leu Ala Glu
          35             40             45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
          50             55             60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
          65             70             75             80

Asp Gly Pro Asp Ile Ile Phe Tyr Ala His Asp Arg Phe Gly Gly Tyr
          85             90             95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
          100            105            110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
          115            120            125

Leu Ile Ala Tyr Pro Ile Ala Val Arg Ala Leu Ser Leu Ile Tyr Asn
          130            135            140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
          145            150            155            160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
          165            170            175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
          180            185            190

Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
          195            200            205

```

Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu
210						215					220				
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu
225					230					235					240
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp
				245					250					255	
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val
			260					265					270		
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu
		275					280					285			
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu
	290					295					300				
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn
305					310					315					320
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu
				325					330					335	
Leu	Ala	Lys	Asp	Pro	Arg	Ala	Ile	Pro	Asn	Asp	Glu	Arg	Asp	Thr	Thr
			340					345					350		
Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu
		355					360					365			
Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala
	370					375					380				
Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp
385					390					395					400
Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile
				405					410					415	
Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile
			420					425					430		
Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile
		435					440					445			
Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro
	450					455					460				
Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg
465					470					475					480
Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser
				485					490					495	
Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu
			500					505					510		

Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu
 515 520 525
 Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro
 530 535 540
 Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys
 545 550 555 560
 Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu
 565 570 575
 Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met
 580 585 590
 Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu
 595 600 605
 Ala Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn
 610 615 620
 Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
 625 630 635 640
 Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
 645 650 655
 Gln Thr Arg Ile Thr Lys
 660

<210> 60
 <211> 1992
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide construct

<400> 60
 atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
 tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
 aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
 gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctgttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttaccgga tcgctgttga agcgttatcg 420
 ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
 ctggataaag aactgaaagc gaaaggtaag agcgcgctga tggtcaacct gcaagaaccg 540
 tacttcacct ggccgctgat tgctgctgac ggggggttatg cggtcaagta tgaaaacggc 600
 aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
 ctgggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaa 720
 gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atggtccaac 780
 atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa gggtaacca 840
 tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
 ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggctctga agcggttaat 960
 aaagacaaac cgctgggtgc cgtagcgtg aagtcttacg aggaagagtt ggcgaaagat 1020

```

ccacgctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg cggtatcatt 1080
gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac gacggggagt 1140
caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc actgattaag 1200
cattggggat ccggcggtgg ccaccagaa acgctggtga aagtaaaaga tgctgaagat 1260
cagttgggtg cagcagtggtg ttacatcgaa ctggatctca acagcggtaa gatccttgag 1320
agttttcgcc ccgaagaacg ttttccaatg atgagcactt ttaaagttct gctatgtggc 1380
gcggtattat cccgtgttga cgccgggcaa gagcaactcg gtcgccgcat acactattct 1440
cagaatgact tggttgagta ctcaccagtc acagaaaagc atcttacgga tggcatgaca 1500
gtaagagaat tatgcagtgc tgccataacc atgagtata acactgcggc caacttactt 1560
ctgacaacga tcggaggacc gaaggagcta accgcttttt tgcacaacat gggggatcat 1620
gtaactcgcc ttgatcggtg ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt 1680
gacaccacga tgcctgcagc aatggcaaca acgttgcgca aactattaac tggcgaacta 1740
cttactctag cttcccgga acaattaata gactggatgg aggcggataa agttgcagga 1800
ccacttctgc gctcgccct tccggctggc tccgccacca tggaaaacgc ccagaaaggt 1860
gaaatcatgc cgaacatccc gcagatgtcc gctttctggt atgccgtgcg tactgcgggtg 1920
atcaacgccg ccagcggtcg tcagactgtc gatgaagccc tgaaagacgc gcagactcgt 1980
atcaccaagt aa 1992

```

<210> 61

<211> 663

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 61

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1                      5                      10                      15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
          20                      25                      30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
          35                      40                      45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
          50                      55                      60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
          65                      70                      75                      80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
          85                      90                      95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
          100                     105                     110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
          115                     120                     125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
          130                     135                     140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
          145                     150                     155                     160

```

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335
 Leu Ala Lys Asp Pro Arg Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly
 340 345 350
 Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys
 355 360 365
 Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met
 370 375 380
 Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys
 385 390 395 400
 His Trp Gly Ser Gly Gly Gly His Pro Glu Thr Leu Val Lys Val Lys
 405 410 415
 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 420 425 430
 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 435 440 445
 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 450 455 460

Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
465 470 475 480

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
485 490 495

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
500 505 510

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
515 520 525

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
530 535 540

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
545 550 555 560

Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
565 570 575

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
580 585 590

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
595 600 605

Ala Gly Ser Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro
610 615 620

Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val
625 630 635 640

Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp
645 650 655

Ala Gln Thr Arg Ile Thr Lys
660

<210> 62

<211> 1992

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 62

```
atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccggtg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgga tcgctgttga agcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatccccggc 480
```

```

ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggg atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa gggtaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
ctggcgaaaag agttcctcga aaactatctg ctgactgatg aaggctctga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg cggatcatt 1080
gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac gacggggagt 1140
caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc actgattaag 1200
cattggggat ccggcggtgg ccaccagaa acgctggtga aagtaaaaga tgctgaagat 1260
cagttgggtg cagcagtggtg ttacatcgaa ctggatctca acagcggtaa gatccttgag 1320
agttttcgcc ccgaagaacg ttttccaatg atgagcaact ttaaagtctt gctatgtggc 1380
gcggtattat cccgtgttga cgccgggcaa gagcaactcg gtcgccgcat acactattct 1440
cagaatgact tggttgagta ctaccagtc acagaaaagc atcttacgga tggcatgaca 1500
gtaagagaat tatgcagtgc tgccataacc atgagtgata acactgcggc caacttactt 1560
ctgacaacga tcggaggacc gaaggagcta accgcttttt tgcacaacat gggggatcat 1620
gtaactcgcc ttgatcggtg ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt 1680
gacaccacga tgctgcagc aatggcaaca acgttgcgca aactattaac tggcgaacta 1740
cttactctag cttcccgga acaattaata gactggatgg aggcggataa agttgcagga 1800
ccacttctgc gctcgccct tccggctggc tccgccacca tggaaaacgc ccagaaaggt 1860
gaatggatgc cgaacatccc gcagatgtcc gctttctggt atgccgtgcg tactgcggtg 1920
atcaacgccg ccagcggtcg tcagactgtc gatgaagccc tgaaagacgc gcagactcgt 1980
atcaccaagt aa 1992

```

<210> 63

<211> 663

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 63

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1             5             10             15

```

```

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20             25             30

```

```

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35             40             45

```

```

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50             55             60

```

```

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65             70             75             80

```

```

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85             90             95

```

```

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100             105             110

```

Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	Ala	Val	Arg	Tyr	Asn	Gly	Lys	115	120	125
Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	Ala	Leu	Ser	Leu	Ile	Tyr	Asn	130	135	140
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala	145	150	155
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn	165	170	175
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly	180	185	190
Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	195	200	205
Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	210	215	220
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	225	230	235
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	245	250	255
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	260	265	270
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	275	280	285
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	290	295	300
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	305	310	315
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	325	330	335
Leu	Ala	Lys	Asp	Pro	Arg	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	340	345	350
Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	355	360	365
Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	370	375	380
Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	385	390	395
His	Trp	Gly	Ser	Gly	Gly	Gly	His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	405	410	415

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 420 425 430
 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 435 440 445
 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 450 455 460
 Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 465 470 475 480
 Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 485 490 495
 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 500 505 510
 Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 515 520 525
 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 530 535 540
 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 545 550 555 560
 Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 565 570 575
 Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 580 585 590
 Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 595 600 605
 Ala Gly Ser Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Trp Met Pro
 610 615 620
 Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val
 625 630 635 640
 Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp
 645 650 655
 Ala Gln Thr Arg Ile Thr Lys
 660

<210> 64

<211> 1992

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic nucleotide construct

<400> 64

```

atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcacccgtt agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggctg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gattgggtac gttacaacgg caagctgatt gcttaccoga tcgctgttga agcggtatcg 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccgcg 480
ctggataaag aactgaaagc gaaaggttaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcggtgat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa gggtaacca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtc gaacaaagag 900
ctggcgaaa agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgtg aagtcttac aggaagagtt ggcgaaagat 1020
ccacgctggt ttattgctga taaatctgga gccggtgagc gtgggtctcg cggatcatt 1080
gcagcactgg ggccagatgg taagccctcc cgtatcgtag ttatctacac gacggggagt 1140
caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgcctc actgattaag 1200
cattggggat ccggcggtgg ccaccagaa acgctggtga aagtaaaaga tgctgaagat 1260
cagttgggtg cacgagtggg ttacatcgaa ctggatctca acagcggtaa gatccttgag 1320
agttttcgcc ccgaagaacg ttttccaatg atgagcactt ttaaagtctt gctatgtggc 1380
gcggtattat cccgtgttga cgccgggcaa gagcaactcg gtcgccgcat acactattct 1440
cagaatgact tggttgagta ctcaccagtc acagaaaagc atcttacgga tggcatgaca 1500
gtaagagaat tatgcagtgc tgccataacc atgagtgata acactgcggc caacttactt 1560
ctgacaacga tcggaggaac gaaggagcta accgcttttt tgcacaacat gggggatcat 1620
gtaactcgcc ttgatcgttg ggaaccggag ctgaatgaag ccataccaaa cgacgagcgt 1680
gacaccacga tgctgcagc aatggcaaca acgttgcgca aactattaac tggcgaaacta 1740
cttactctag cttcccgga acaattaata gactggatgg aggcggataa agttgcagga 1800
ccacttctgc gtcggccct tccggctggc tccgccacca tggaaaacgc ccagaaaggt 1860
gaatggatgc cgaacatccc gcagatgtcc gctttctggt atgccgtgcg tactgcggtg 1920
atcaacgccg ccagcggtcg tcagactgtc gatgaagccc tgaaagacgc gcagactcgt 1980
atcaccaagt aa 1992

```

<210> 65

<211> 663

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 65

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1                      5                      10                      15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20                      25                      30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35                      40                      45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50                      55                      60

```


His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	Pro	Gln	Val	Ala	Ala	Thr	Gly	
65					70					75					80	
Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala	His	Asp	Arg	Phe	Gly	Gly	Tyr	
				85					90					95		
Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	Thr	Pro	Asp	Lys	Ala	Phe	Gln	
			100					105					110			
Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	Trp	Val	Arg	Tyr	Asn	Gly	Lys	
		115					120					125				
Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	Ala	Leu	Ser	Leu	Ile	Tyr	Asn	
	130					135					140					
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala	
145					150					155					160	
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn	
				165					170					175		
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly	
			180					185					190			
Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	
	195						200					205				
Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	
	210					215					220					
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	
225					230					235					240	
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	
			245						250					255		
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	
			260					265					270			
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	
		275					280					285				
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	
	290					295					300					
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	
305					310					315					320	
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	
				325					330					335		
Leu	Ala	Lys	Asp	Pro	Arg	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	
			340					345					350			
Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	
		355					360					365				

<210> 66
 <211> 1989
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide construct

<400> 66
 atgaaaataa aaacaggtgc acgcatcctc gcattatccg cattaacgac gatgatgttt 60
 tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
 aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
 gtcaccgttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctggttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttaccoga tcgctgttga agcgttatcg 420
 ctggataaag aactgaaagc gctgccgaac ccgccaaaaa cctgggaaga gatcccgcg 480
 ctgtgataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
 tacttcacct ggccgctgat tgctgctgac gggcatctta cggatggcat gacagtaaga 600
 gaattatgca gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca 660
 acgatcggag gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact 720
 cgccttgatc gttgggaacc ggaactgaat gaagccatac caaacgacga gcgtgacacc 780
 acgatgcctg cagcaatggc aacaacgttg cgaaactat taactggcga actacttact 840
 ctagcttccc ggcaacaatt aatagactgg atggaggcgg ataaagtgc aggaccactt 900
 ctgcgctcgg cccttccggc tggctggttt attgctgata aatctggagc cggtgagcgt 960
 gggctctcgg gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagtt 1020
 atctacacga cggggagtca ggcaactatg gatgaacgaa atagacagat cgctgagata 1080
 ggtgcctcac tgattaaagca ttgggacaag agccaccag aaacgctggt gaaagtaaaa 1140
 gatgctgaag atcagttggg tgcacgagtg gggtacatcg aactggatct caacagcgg 1200
 aagatccttg agagttttcg ccccgaagaa cgttttccaa tgatgagcac ttttaaagtt 1260
 ctgctatgtg gcgcggtatt atcccgtgtt gacgcggggc aagagcaact cggtcgccgc 1320
 atacactatt ctacagaatga cttggttgag tactcaccag tcacagacgg gggttatgcg 1380
 ttcaagtatg aaaacggcaa gtacgacatt aaagacgtgg gcgtggataa cgctggcgcg 1440
 aaagcgggtc tgaccttccct ggttgacctg attaaaaaca aacacatgaa tgcagacacc 1500
 gattactcca tcgcagaagc tgcctttaat aaaggcgaaa cagcgatgac catcaacggc 1560
 ccgtgggcat ggtccaacat cgacaccagc aaagtgaatt atggtgtaac ggtactgccc 1620
 accttcaagg gtcaaccatc caaaccgttc gttggcgtgc tgagcgcagg tattaacgcc 1680
 gccagtccga acaaagagct ggcgaaagag ttctcgaaaa actatctgct gactgatgaa 1740
 ggtctggaag cggttaataa agacaaaccg ctgggtgccc tagcgtgaa gtcttacgag 1800
 gaagagttgg cgaaagatcc acgtattgcc gccaccatgg aaaacgcca gaaaggtgaa 1860
 atcatgccga acatcccga gatgtccgct ttctggtatg ccgtgcgtac tgcggtgate 1920
 aacgcgcga gcggtcgtca gactgtcgat gaagccctga aagacgcga gactcgtatc 1980
 accaagtaa 1989

<210> 67
 <211> 662
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 protein construct

<400> 67
 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1 5 10 15

Thr	Met	Met	Phe	Ser	Ala	Ser	Ala	Leu	Ala	Lys	Ile	Glu	Glu	Gly	Lys		
			20					25						30			
Leu	Val	Ile	Trp	Ile	Asn	Gly	Asp	Lys	Gly	Tyr	Asn	Gly	Leu	Ala	Glu		
		35					40					45					
Val	Gly	Lys	Lys	Phe	Glu	Lys	Asp	Thr	Gly	Ile	Lys	Val	Thr	Val	Glu		
	50					55					60						
His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	Pro	Gln	Val	Ala	Ala	Thr	Gly		
	65				70					75					80		
Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala	His	Asp	Arg	Phe	Gly	Gly	Tyr		
				85					90					95			
Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	Thr	Pro	Asp	Lys	Ala	Phe	Gln		
			100					105					110				
Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	Ala	Val	Arg	Tyr	Asn	Gly	Lys		
		115					120					125					
Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	Ala	Leu	Ser	Leu	Ile	Tyr	Asn		
	130					135					140						
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala		
	145				150					155					160		
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn		
				165				170						175			
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	His		
			180					185					190				
Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	Ala	Ile	Thr		
		195					200					205					
Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	Ile	Gly	Gly		
	210					215					220						
Pro	Lys	Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	Gly	Asp	His	Val	Thr		
	225				230					235					240		
Arg	Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	Ala	Ile	Pro	Asn	Asp		
				245					250					255			
Glu	Arg	Asp	Thr	Thr	Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys		
			260					265					270				
Leu	Leu	Thr	Gly	Glu	Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile		
		275					280					285					
Asp	Trp	Met	Glu	Ala	Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala		
	290					295					300						
Leu	Pro	Ala	Gly	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg		
	305				310					315					320		

Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser		
				325					330					335			
Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu		
			340					345					350				
Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp		
		355					360					365					
Asp	Lys	Ser	His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp		
	370					375					380						
Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly		
385					390					395					400		
Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser		
				405					410					415			
Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly	Ala	Val	Leu	Ser	Arg	Val	Asp	Ala		
			420					425					430				
Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg	Ile	His	Tyr	Ser	Gln	Asn	Asp	Leu		
		435					440					445					
Val	Glu	Tyr	Ser	Pro	Val	Thr	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	Tyr	Glu		
	450					455					460						
Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	Gly	Ala		
465					470					475					480		
Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	His	Met		
				485					490					495			
Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	Lys	Gly		
			500					505					510				
Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	Ile	Asp		
		515					520					525					
Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	Lys	Gly		
	530					535					540						
Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	Ser	Ala	Gly	Ile	Asn	Ala		
545					550					555					560		
Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	Phe	Leu	Glu	Asn	Tyr	Leu		
				565					570					575			
Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	Lys	Asp	Lys	Pro	Leu	Gly		
			580					585					590				
Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	Leu	Ala	Lys	Asp	Pro	Arg		
		595					600					605					
Ile	Ala	Ala	Thr	Met	Glu	Asn	Ala	Gln	Lys	Gly	Glu	Ile	Met	Pro	Asn		
	610					615					620						

Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile
 625 630 635 640

Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala
 645 650 655

Gln Thr Arg Ile Thr Lys
 660

<210> 68
 <211> 1995
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide construct

<400> 68
 atgaaaataa aaacagggtgc acgcatcctc gcattatccg cattaacgac gatgatgttt 60
 tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
 aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
 gtcaccggtt agcatccgga taaactggaa gagaaattcc cacagggtgc ggcaactggc 240
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctggttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgcccgtac gttacaacgg caagctgatt gcttaccoga tcgctgttga agcgttatcg 420
 ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccgcg 480
 ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
 tacttcacct ggccgctgat tgctgctgac gggcttctgc gctcggccct tccggtggc 600
 tgggtttatt ctgataaatc tggagccggt gagcgtgggt ctgcggtat cattgcagca 660
 ctggggccag atggttaagc ctcccgtatc gtagttatct acacgacggg gagtcaggca 720
 actatggatg aacgaaatag acagatcgct gagatagggt cctcactgat taagcattgg 780
 ggatccggcg gtggccaccc agaaacgctg gtgaaagtaa aagatgctga agatcagttg 840
 ggtgcacgag tgggttacat cgaactggat ctcaacagcg gtaagatcct tgagagtttt 900
 cgccccgaag aacgttttcc aatgatgagc acttttaaaag ttctgctatg tggcgcggtg 960
 ttatcccggt ttgacgcggg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat 1020
 gacttgggtg agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga 1080
 gaattatgca gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca 1140
 acgatcggag gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact 1200
 cgccttgatc gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc 1260
 acgatgcctg cagcaatggc aacaacgttg cgcaaactat taactggcga actacttact 1320
 ctagcttccc ggcaacaatt aatagactgg atggaggcgg ataaagtgtg agacgggggt 1380
 tatgcgttca agtatgaaaa cggcaagtac gacattaaag acgtgggctg ggataacgct 1440
 ggcgcgaaa ggggtctgac cttcctggtt gacctgatta aaaacaaaca catgaatgca 1500
 gacaccgatt actccatcgc agaagctgcc tttaataaa gcgaaacagc gatgaccatc 1560
 aacggcccggt gggcatggtc caacatcgac accagcaaa gtaattatgg tgtaacggta 1620
 ctgccgacct tcaagggtca accatccaaa ccgttcgttg gcgtgctgag cgcagggtatt 1680
 aacgccgcca gtccgaacaa agagctggcg aaagagttcc tcgaaaacta tctgctgact 1740
 gatgaagggtc tggaagcggg taataaagac aaaccgctgg gtgccgtagc gctgaagtct 1800
 tacgaggaag agttggcgaa agatccacgt attgccgcca ccatggaaaa cgcccagaaa 1860
 ggtgaaatca tgccgaacat cccgcagatg tccgctttct ggtatgccgt gcgtactgcg 1920
 gtgatcaacg ccgccagcgg tcgtcagact gtcgatgaag ccctgaaaga cgcgcagact 1980
 cgtatcacca agtaa 1995

<210> 69
 <211> 664
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 protein construct

<400> 69
 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 1 5 10 15
 Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 20 25 30
 Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
 35 40 45
 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 50 55 60
 His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 65 70 75 80
 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 85 90 95
 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 100 105 110
 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 115 120 125
 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 130 135 140
 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 145 150 155 160
 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Leu
 180 185 190
 Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly
 195 200 205
 Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp
 210 215 220
 Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala
 225 230 235 240
 Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu
 245 250 255

Ile	Lys	His	Trp	Gly	Ser	Gly	Gly	Gly	His	Pro	Glu	Thr	Leu	Val	Lys	260	265	270	
Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr	Ile	Glu	275	280	285	
Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro	Glu	Glu	290	295	300	
Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly	Ala	Val	305	310	315	320
Leu	Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg	Ile	His	325	330	335	
Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	Glu	Lys	His	340	345	350	
Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	Ala	Ile	Thr	355	360	365	
Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	Ile	Gly	Gly	370	375	380	
Pro	Lys	Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	Gly	Asp	His	Val	Thr	385	390	395	400
Arg	Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	Ala	Ile	Pro	Asn	Asp	405	410	415	
Glu	Arg	Asp	Thr	Thr	Met	Pro	Ala	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	420	425	430	
Leu	Leu	Thr	Gly	Glu	Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	435	440	445	
Asp	Trp	Met	Glu	Ala	Asp	Lys	Val	Ala	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	450	455	460	
Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	465	470	475	480
Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	485	490	495	
His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	500	505	510	
Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	515	520	525	
Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	530	535	540	
Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	Ser	Ala	Gly	Ile	545	550	555	560

Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn
 565 570 575
 Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro
 580 585 590
 Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp
 595 600 605
 Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met
 610 615 620
 Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala
 625 630 635 640
 Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys
 645 650 655
 Asp Ala Gln Thr Arg Ile Thr Lys
 660

<210> 70

<211> 2004

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence: Synthetic
 nucleotide construct

<400> 70

```

atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccggtg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgga tcgctgttga agcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac gggaatgaag ccataccaaa cgacgagcgt 600
gacaccacga tgcctgcagc aatggcaaca acgttgcgca aactattaac tggcgaacta 660
cttactctag cttcccggca acaattaata gactggatgg aggcggataa agttgcagga 720
ccacttctgc gctcggccct tccggtcggc tggtttattg ctgataaatc tggagccggt 780
gagcgtgggt ctgcggtat cattgcagca ctggggccag atggtaagcc ctcccgtatc 840
gtagttatct acacgacggg gagtcaggca actatggatg aacgaaatag acagatcgct 900
gagataggtg cctcactgat taagcattgg gacaagagcc acccagaaac gctggtgaaa 960
gtaaaagatg ctgaagatca gttgggtgca cgagtgggtt acatcgaact ggatctcaac 1020
agcggtaaga tccttgagag ttttcgcccc gaagaacgtt ttccaatgat gagcactttt 1080
aaagttctgc tatgtggcgc ggtattatcc cgtgttgacg ccgggcaaga gcaactcggg 1140
cgccgcatac actattctca gaatgacttg gttgagtact caccagtcac agaaaagcat 1200
cttacggatg gcatgacagt aagagaatta tgcagtgctg ccataaccat gagtgataac 1260
actgcggcca acttacttct gacaacgatc ggaggaccga aggagctaac cgcttttttg 1320
cacaacatgg gggatcatgt aactcgcctt gatcgttggg aaccggaact gaatgaagcc 1380
gacggggggt atgcgttcaa gtatgaaaac ggcaagtacg acattaaaga cgtgggcgtg 1440
gataacgctg gcgcgaaagc gggctctgacc ttccctggtg acctgattaa aaacaaacac 1500
atgaatgcag acaccgatta ctccatcgca gaagctgcct ttaataaagg cgaaacagcg 1560

```

```

atgaccatca acggcccgtg ggcattgtcc aacatcgaca ccagcaaagt gaattatggt 1620
gtaacgggtac tgccgacctt caaggggtcaa ccatccaaac cgttcggttg cgtgctgagc 1680
gcaggtatta acgcccgcag tccgaacaaa gagctggcga aagagttcct cgaaaactat 1740
ctgctgactg atgaagggtt ggaagcgggt aataaagaca aaccgctggg tgccgtagcg 1800
ctgaagtctt acgaggaaga gttggcgaaa gatccacgta ttgccgccac catggaaaac 1860
gcccagaaaag gtgaaatcat gccgaacatc ccgcagatgt ccgctttctg gtatgccgtg 1920
cgtactgcgg tgatcaacgc cgccagcggg cgtcagactg tcgatgaagc cctgaaagac 1980
gcgcagactc gtatcaccaa gtaa                                2004

```

<210> 71

<211> 667

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 71

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1                      5                      10                      15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20                      25                      30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35                      40                      45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50                      55                      60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65                      70                      75                      80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85                      90                      95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100                      105                      110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
      115                      120                      125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
      130                      135                      140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
      145                      150                      155                      160

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
      165                      170                      175

Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Asn
      180                      185                      190

Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Ala Ala Met
      195                      200                      205

```

Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu	Leu	Leu	Thr	Leu	Ala	210	215	220	
Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala	Asp	Lys	Val	Ala	Gly	225	230	235	240
Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	Phe	Ile	Ala	Asp	Lys	245	250	255	
Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	260	265	270	
Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	275	280	285	
Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	290	295	300	
Ser	Leu	Ile	Lys	His	Trp	Asp	Lys	Ser	His	Pro	Glu	Thr	Leu	Val	Lys	305	310	315	320
Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr	Ile	Glu	325	330	335	
Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro	Glu	Glu	340	345	350	
Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly	Ala	Val	355	360	365	
Leu	Ser	Arg	Val	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg	Ile	His	370	375	380	
Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	Glu	Lys	His	385	390	395	400
Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	Ala	Ile	Thr	405	410	415	
Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	Ile	Gly	Gly	420	425	430	
Pro	Lys	Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	Gly	Asp	His	Val	Thr	435	440	445	
Arg	Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	Ala	Asp	Gly	Gly	Tyr	450	455	460	
Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	465	470	475	480
Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	485	490	495	
Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	500	505	510	

Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp Ala
515 520 525

Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val Leu
530 535 540

Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu Ser
545 550 555 560

Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu Phe
565 570 575

Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn Lys
580 585 590

Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu Leu
595 600 605

Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys Gly
610 615 620

Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala Val
625 630 635 640

Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp Glu
645 650 655

Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys
660 665

<210> 72

<211> 2001

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<400> 72

```

atgaaaataa aaacaggtgc acgcatcctc gcattatccg cattaacgac gatgatgttt 60
tccgcctcgg ctctcgccaa aatcgaagaa ggtaaaactgg taatctggat taacggcgat 120
aaaggctata acggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
gtcaccggtg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
ctgttggtcg aaatcacccc ggacaaaagcgt ttccaggaca agctgtatcc gtttacctgg 360
gatgccgtac gttacaacgg caagctgatt gcttaccgga tgcgtgttga agcgttatcg 420
ctgatttata acaaagatct gctgccgaac ccgcaaaaaa cctgggaaga gatcccggcg 480
ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac ggggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgcagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggc atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa ggggtcaaaca 840
tccaaaccgt tcgttggcgt gctgagcgca ggtattaacg ccgccagtc gaacaaagag 900
ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgtg aagtcttacg aggaagagtt ggcgaaagat 1020

```

```

ccacgtattg cgcgccaccat ggaaaacgcc cagaaagggtg aaatcatgcc gaacatcccg 1080
cagatgtccg ctttctggta tgccgtgcgt actgcggtga tcaacgccgc cagcgggtcgt 1140
cagactgtcg atgaagccct gaaagacgcg cagactcgta tcaccaaggg catgacagta 1200
agagaattat gcagtgtcgc cataaccatg agtgataaca ctgcggccaa cttacttctg 1260
acaacgatcg gaggaccgaa ggagctaacc gcttttttgc acaacatggg ggatcatgta 1320
actcgccttg atcgttggga accggagctg aatgaagcca taccaaacga cgagcgtgac 1380
accacgatgc ctgcagcaat ggcaacaacg ttgcgcaaac tattaactgg cgaactactt 1440
actctagctt cccggcaaca attaatagac tggatggagg cggataaagt tgcaggacca 1500
cttctgcgct cggcccttcc ggctggctgg tttattgctg ataaatctgg agccggtgag 1560
cgtgggtctc gcggtatcat tgcagcactg gggccagatg gtaagccctc ccgtatcgta 1620
gttatctaca cgacggggag tcaggcaact atggatgaac gaaatagaca gatcgtctgag 1680
ataggtgcct cactgattaa gcattgggga tccggcggtg gccaccaga aacgctggtg 1740
aaagtaaaag atgctgaaga tcagttgggt gcacgagtgg gttacatcga actggatctc 1800
aacagcggta agatccttga gagttttcgc cccgaagaac gttttccaat gatgagcact 1860
tttaaagttc tgctatgtgg cgcggtatta tcccggtgtg acgccgggca agagcaactc 1920
ggtcgcgcga tacactattc tcagaatgac ttggttgagt actcaccagt cacagaaaag 1980
catcttacgg atggcaagtg a                                     2001

```

<210> 73

<211> 666

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 73

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1                      5                      10                      15

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
                20                      25                      30

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
                35                      40                      45

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
  50                      55                      60

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
  65                      70                      75                      80

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
                85                      90                      95

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
  100                      105                      110

Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
  115                      120                      125

Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
  130                      135                      140

Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
  145                      150                      155                      160

```

Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 165 170 175
 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 180 185 190
 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 195 200 205
 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 210 215 220
 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 225 230 235 240
 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 245 250 255
 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 260 265 270
 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 275 280 285
 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 290 295 300
 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 305 310 315 320
 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
 325 330 335
 Leu Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys
 340 345 350
 Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala
 355 360 365
 Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp
 370 375 380
 Glu Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys Gly Met Thr Val
 385 390 395 400
 Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala
 405 410 415
 Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe
 420 425 430
 Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro
 435 440 445
 Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro
 450 455 460

Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu
 465 470 475 480

Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys
 485 490 495

Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile
 500 505 510

Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala
 515 520 525

Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr
 530 535 540

Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu
 545 550 555 560

Ile Gly Ala Ser Leu Ile Lys His Trp Gly Ser Gly Gly Gly His Pro
 565 570 575

Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg
 580 585 590

Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser
 595 600 605

Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu
 610 615 620

Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu
 625 630 635 640

Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro
 645 650 655

Val Thr Glu Lys His Leu Thr Asp Gly Lys
 660 665

<210> 74

<211> 2010

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 nucleotide construct

<400> 74

atgaaaataa aaacaggtgc acgcatacctc gcattatccg cattaacgac gatgatgttt 60
 tccgcctcgg ctctcgccaa aatcgaagaa ggtaaacctgg taatctggat taacggcgat 120
 aaaggctata acgggtctcgc tgaagtcggt aagaaattcg agaaagatac cggaattaaa 180
 gtcaccggttg agcatccgga taaactggaa gagaaattcc cacaggttgc ggcaactggc 240
 gatggccctg acattatctt ctgggcacac gaccgctttg gtggctacgc tcaatctggc 300
 ctgttggtg aaatcacccc ggacaaagcg ttccaggaca agctgtatcc gtttacctgg 360
 gatgccgtac gttacaacgg caagctgatt gcttaccgca tcgctgttga agcgttatcg 420
 ctgatttata acaaagatct gctgccgaac ccgccaaaaa cctgggaaga gatcccggcg 480

```

ctggataaag aactgaaagc gaaaggtaag agcgcgctga tgttcaacct gcaagaaccg 540
tacttcacct ggccgctgat tgctgctgac gggggttatg cgttcaagta tgaaaacggc 600
aagtacgaca ttaaagacgt gggcgtggat aacgctggcg cgaaagcggg tctgaccttc 660
ctggttgacc tgattaaaaa caaacacatg aatgcagaca ccgattactc catcgagaa 720
gctgccttta ataaaggcga aacagcgatg accatcaacg gcccggtggg atggtccaac 780
atcgacacca gcaaagtga ttatggtgta acggtactgc cgaccttcaa gggtaacca 840
tccaaaccgt tcgttgccgt gctgagcgca ggtattaacg ccgccagtcc gaacaaagag 900
ctggcgaaag agttcctcga aaactatctg ctgactgatg aaggtctgga agcggttaat 960
aaagacaaac cgctgggtgc cgtagcgctg aagtcttacg aggaagagtt ggcgaaagat 1020
ccacgtattg ccgccaccat ggaaaacgcc cagaaagggtg aaatcatgcc gaacatccc 1080
cagatgtccg ctttctggta tgccgtgcgt actgcggtga tcaacgccgc cagcggtcgt 1140
cagactgtcg atgaagccct gaaagacgcg cagactcgta tcaccaaggg catgacagta 1200
agagaattat gcagtgtctg cataaccatg agtgataaca ctgcggccaa cttacttctg 1260
acaacgatcg gaggaccgaa ggagctaacc gcttttttgc acaacatggg ggatcatgta 1320
actcgccttg atcgttgga accggagctg aatgaagcca taccaaacga cgagcgtgac 1380
accacgatgc ctgcagcaat ggcaacaacg ttgcgcaaac tattaactgg cgaactactt 1440
actctagctt cccggcaaca attaatagac tggatggagg cggataaagt tgcaggacca 1500
cttctgcgct cgcccttcc ggctggctgg tttattgctg ataaatctgg agccggtgag 1560
cgtgggtctc cggtatcat tgcagcactg gggccagatg gtaagccctc ccgtatcgta 1620
gttatctaca cgacggggag tcaggcaact atggatgaac gaaatagaca gatcgctgag 1680
ataggtgcct cactgattaa gcattgggga tccggcggtg gccaccaga aacgctggtg 1740
aaagtaaaag atgctgaaga tcagttgggt gcacgagtgg gttacatcga actggatctc 1800
aacagcggta agatccttga gagttttcgc cccgaagaac gttttccaat gatgagcact 1860
tttaaagttc tgctatgtgg cgcggtatta tcccggtgtg acgccgggca agagcaactc 1920
ggtcgcgcga tacactattc tcagaatgac ttggttgagt actcaccagt cacagaaaag 1980
catcttacgg aagtgaagag cactagttag 2010

```

<210> 75

<211> 669

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic protein construct

<400> 75

```

Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
  1                      5                      10                      15

```

```

Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
      20                      25                      30

```

```

Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
      35                      40                      45

```

```

Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
      50                      55                      60

```

```

His Pro Asp Lys Leu Glu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
      65                      70                      75                      80

```

```

Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
      85                      90                      95

```

```

Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
      100                      105                      110

```


Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	Ala	Val	Arg	Tyr	Asn	Gly	Lys	115	120	125
Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	Ala	Leu	Ser	Leu	Ile	Tyr	Asn	130	135	140
Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	Thr	Trp	Glu	Glu	Ile	Pro	Ala	145	150	155
Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	Lys	Ser	Ala	Leu	Met	Phe	Asn	165	170	175
Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	Leu	Ile	Ala	Ala	Asp	Gly	Gly	180	185	190
Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	Tyr	Asp	Ile	Lys	Asp	Val	Gly	195	200	205
Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	Leu	Thr	Phe	Leu	Val	Asp	Leu	210	215	220
Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	Thr	Asp	Tyr	Ser	Ile	Ala	Glu	225	230	235
Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	Met	Thr	Ile	Asn	Gly	Pro	Trp	245	250	255
Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	Val	Asn	Tyr	Gly	Val	Thr	Val	260	265	270
Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	Lys	Pro	Phe	Val	Gly	Val	Leu	275	280	285
Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	Asn	Lys	Glu	Leu	Ala	Lys	Glu	290	295	300
Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	Glu	Gly	Leu	Glu	Ala	Val	Asn	305	310	315
Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	Leu	Lys	Ser	Tyr	Glu	Glu	Glu	325	330	335
Leu	Ala	Lys	Asp	Pro	Arg	Ile	Ala	Ala	Thr	Met	Glu	Asn	Ala	Gln	Lys	340	345	350
Gly	Glu	Ile	Met	Pro	Asn	Ile	Pro	Gln	Met	Ser	Ala	Phe	Trp	Tyr	Ala	355	360	365
Val	Arg	Thr	Ala	Val	Ile	Asn	Ala	Ala	Ser	Gly	Arg	Gln	Thr	Val	Asp	370	375	380
Glu	Ala	Leu	Lys	Asp	Ala	Gln	Thr	Arg	Ile	Thr	Lys	Gly	Met	Thr	Val	385	390	395
Arg	Glu	Leu	Cys	Ser	Ala	Ala	Ile	Thr	Met	Ser	Asp	Asn	Thr	Ala	Ala	405	410	415

Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe
 420 425 430
 Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro
 435 440 445
 Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro
 450 455 460
 Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu
 465 470 475 480
 Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys
 485 490 495
 Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile
 500 505 510
 Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala
 515 520 525
 Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr
 530 535 540
 Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu
 545 550 555 560
 Ile Gly Ala Ser Leu Ile Lys His Trp Gly Ser Gly Gly Gly His Pro
 565 570 575
 Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg
 580 585 590
 Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser
 595 600 605
 Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu
 610 615 620
 Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly Gln Glu Gln Leu
 625 630 635 640
 Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro
 645 650 655
 Val Thr Glu Lys His Leu Thr Glu Val Lys Ser Thr Ser
 660 665

<210> 76

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 76
ggaccaggat ccatgaaaat aaaaacaggt

30

<210> 77
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 77
Gly Gly Ser Gly His His His His His His His His
1 5 10

<210> 78
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 78
gctcttctca cccagaaacg ctggtg

26

<210> 79
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 79
ctgattaagc attgggacaa gagccactga agaga

35

<210> 80
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 80
cacccagaaa cgctggtg

18

<210> 81
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 81
 ctgattaagc attgggacaa gagc 24

<210> 82
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 82
 gtggctcttg tcccaatgct taatcag 27

<210> 83
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 83
 caccagcgtt tctgg 15

<210> 84
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 84
 ctgattaagc attgggacaa gagccaccca gaaacgctgg tg 42

<210> 85
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 85
ggatccggcg gtggccaccc agaaacgctg gtg 33

<210> 86
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 86
ctgattaagc attggggatc c 21

<210> 87
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 87
gatccggcgg tggccacca gaaacgctgg tg 32

<210> 88
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 88
ctgattaagc attggg 16

<210> 89
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 89
gatccccaat gcttaatcag 20

<210> 90
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 90
caccagcggtt tctgggtggc caccgccg

28

<210> 91
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 91
ctgattaagc attgggggatc cggcgggtggc caccagaaa cgctggtg

48

<210> 92
<211> 59
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 92
ctgattgctg ctgacgggtg aagagcgctc gaggtctctc cgacgggggt tatgcgttc

59

<210> 93
<211> 15
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 93
ctgattgctg ctgac

15

<210> 94
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 94
gacggggggtt atgcgttc 18

<210> 95
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 95
gaacgcataa ccccc 15

<210> 96
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 96
cccgtcagca gcaatcag 18

<210> 97
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 97
ctgattgctg ctgacggg 18

<210> 98
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 98
ctgatcgcta ggagacggcg a

21

<210> 99
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
6xHis tag

<400> 99
His His His His His His
1 5